Remarks

Upon entry of the foregoing amendment, claims 1-46 are pending in the application, with claims 1, 14, 32, 34, 38, 40, 41 and 44 being the independent claims. Applicants have amended claim 31 to make it dependent on claim 14. Support for the amendment to claim 31 may be found, *inter alia*, in Example 39. These changes are believed to introduce no new matter, and their entry is respectfully requested.

Election

The Examiner requested an election of an invention directed to one of the following of Groups I-DXCI. Groups CCLXXXI-CCCVI, corresponding to claims 14-15 and 19-30 and newly amended claim 31, are drawn to a method of identifying potentially therapeutic anticancer compounds comprising contacting one Transferrin Receptor Related Apoptosis Inducing Protein with test compounds, wherein compounds that bind one Transferrin Receptor Related Apoptosis Inducing Protein are potentially therapeutic anticancer compound. The Examiner has requested an election of one Transferrin Receptor Related Apoptosis Inducing Protein, corresponding to one of SEQ ID NOS:1-26.

Applicants hereby provisionally elect to prosecute the invention of Group CCLXXXI, represented by claims 14-15 and 19-30 and newly amended claim 31. Applicants further elect SEQ ID NO:1 and the species 1-(3-methyl-2-butenyl)-3,3-dimethyl-1,3,3a,4,5,12a-hexahydro-7,13-dioxo-1,5-methano-furo[3,4-d]xanthene of

claim 31. This election is made without prejudice to or disclaimer of the other claims or inventions disclosed.

This election is made with traverse.

Applicants respectfully request rejoinder of groups CCLXXXI-CCCVI. While the Examiner has required election of one of SEQ ID NOS:1-26 for prosecution, Applicants respectfully point out to the Examiner that SEQ ID NOS:1-26 are related sequences. Applicants attach herewith sequence alignments of SEQ ID NO:1 and SEQ ID NOS:2-26 generated by BLAST (Basic Local Alignment Search Tool). As seen from the alignments, SEQ ID NOS:1, 2, 3 and 8 are identical sequences. Further, there is only one amino acid difference between SEQ ID NO:1 and SEQ ID NOS:4, 5, 6, 9 and 10. Further, SEQ ID NOS:11-21 are fragments of 639 or 640 amino acids in length and have one or three amino acid differences (greater than 99% identical) compared with the corresponding fragments in SEQ ID NO:1. Therefore, at a minimum, Applicants request that the Examiner rejoin Groups CCLXXXII-CCLXXXVI and CCLXXXVIII-CCXC (corresponding to SEQ ID NOS:2-6 and SEQ ID NOS:8-10) with Group CCLXXXI, because the sequences are identical or differ by only one amino acid and would therefore involve the same search. Likewise, Groups CCXCI-CCCI (corresponding to SEQ ID NOS:11-21) should be rejoined with Group CCLXXXI on the same basis. SEQ ID NOS:7 and 22-26 are smaller fragments of 15-63 amino acids and share from 81-100% identity with the corresponding fragments of SEQ ID NO:1. Therefore, a search of SEQ ID NO:1 would necessarily be coextensive with a search for these sequences as well and

Applicants respectfully request rejoinder of Groups CCLXXXVII and CCCII-CCCVI with Group CCLXXXI.

Reconsideration and withdrawal of the Restriction Requirement, and consideration and allowance of all pending claims, are respectfully requested. It is not believed that extensions of time are required, beyond those that may otherwise be provided for in accompanying documents. However, if additional extensions of time are necessary to prevent abandonment of this application, then such extensions of time are hereby petitioned under 37 C.F.R. § 1.136(a), and any fees required therefor are hereby authorized to be charged to our Deposit Account No. 19-0036.

Respectfully submitted,

STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

Robert W. Esmond

Robert W. Esmond
Attorney for Applicants
Registration No. 32,893

Date: Nov. 20, 2006

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Washington, D.C. 20005-3934
(202) 371-2600

599905_1.DOC

NCBI Blast 2 Sequences results

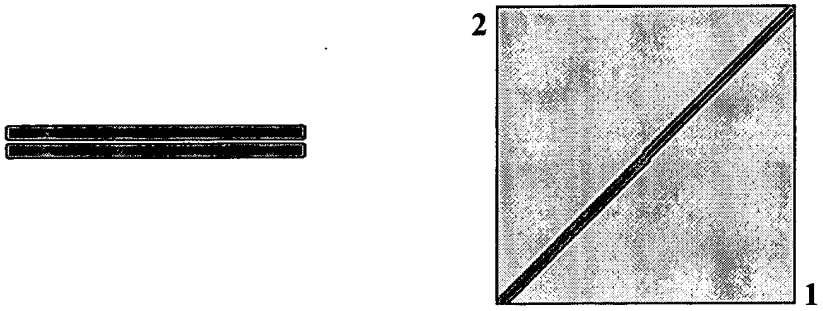
PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☑ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)

Sequence 2: gi|6164848|gb|AAF04564.1|AF187320_1transferrin receptor [Homo sapiens] >gi|108935939|sp|P02786|TFR1_HUMAN Transferrin receptor protein 1 (TfR1) (TR) (TfR) (Trfr) (CD71 antigen) (T9) (p90) >gi|12654697|gb|AAH01188.1| TFRC protein [Homo sapiens] >gi|94717625|gb|ABF47088.1| transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

Score = 1531 bits (3964), Expect = 0.0
Identities = 760/760 (100%), Positives = 760/760 (100%), Gaps = 0/760 (0%)

SEQUENCE:
1
2

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Query  1    MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK  60
            MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK
Sbjct  1    MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK  60

Query  61   RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR  120
            RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR
Sbjct  61   RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR  120

Query  121  RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK  180
            RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK
Sbjct  121  RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK  180
```

```
Query  181  VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK  240
            VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK
Sbjct  181  VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK  240

Query  241  KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH  300
            KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH
Sbjct  241  KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH  300

Query  301  AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD  360
            AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD
Sbjct  301  AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD  360

Query  361  STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG  420
            STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
Sbjct  361  STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG  420

Query  421  VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT  480
            VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
Sbjct  421  VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT  480

Query  481  YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA  540
            YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
Sbjct  481  YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA  540

Query  541  AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK  600
            AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
Sbjct  541  AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK  600

Query  601  LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF  660
            LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
Sbjct  601  LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF  660

Query  661  GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK  720
            GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
Sbjct  661  GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK  720

Query  721  QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  760
            QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct  721  QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  760


CPU time:     0.04 user secs.       0.02 sys. secs          0.06 total secs.

Lambda     K      H
   0.318    0.135    0.399

Gapped
Lambda     K      H
   0.267   0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 4468
Number of extensions: 2537
Number of successful extensions: 1
Number of sequences better than 10.0: 1
```

```
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,435,209,301
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,435,209,158
Effective search space: 885524050486
Effective search space used: 885524050486
Neighboring words threshold: 9
X1: 16 ( 7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)
```

Blast 2 Sequences results

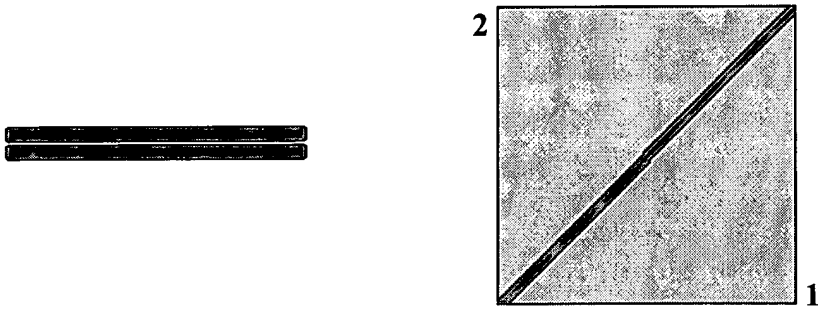
PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☑ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)

Sequence 2: gi|12654697|gb|AAH01188.1|TFRC protein [Homo sapiens]
>gi|108935939|sp|P02786|TFR1_HUMAN Transferrin receptor protein 1 (TfR1) (TR) (TfR) (Trfr) (CD71 antigen) (T9) (p90) >gi|6164848|gb|AAF04564.1|AF187320_1 transferrin receptor [Homo sapiens] >gi|94717625|gb|ABF47088.1| transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

Score = 1531 bits (3964), Expect = 0.0
Identities = 760/760 (100%), Positives = 760/760 (100%), Gaps = 0/760 (0%)

SEQ ID NO

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1   Query  1    MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK  60
           MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK
3   Sbjct  1    MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK  60

    Query  61   RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR  120
           RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR
    Sbjct  61   RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR  120

    Query  121  RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK  180
           RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK
    Sbjct  121  RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK  180
```

```
Query  181  VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK  240
            VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK
Sbjct  181  VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK  240

Query  241  KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH  300
            KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH
Sbjct  241  KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH  300

Query  301  AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAAEKLFGNMEGDCPSDWKTD  360
            AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAAEKLFGNMEGDCPSDWKTD
Sbjct  301  AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAAEKLFGNMEGDCPSDWKTD  360

Query  361  STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG  420
            STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
Sbjct  361  STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG  420

Query  421  VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT  480
            VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
Sbjct  421  VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT  480

Query  481  YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA  540
            YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
Sbjct  481  YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA  540

Query  541  AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK  600
            AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
Sbjct  541  AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK  600

Query  601  LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF  660
            LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
Sbjct  601  LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF  660

Query  661  GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK  720
            GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
Sbjct  661  GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK  720

Query  721  QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  760
            QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct  721  QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  760


CPU time:     0.03 user secs.       0.01 sys. secs          0.04 total secs.

Lambda     K      H
   0.318    0.135    0.399

Gapped
Lambda     K      H
   0.267   0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 4468
Number of extensions: 2537
Number of successful extensions: 1
Number of sequences better than 10.0: 1
```

```
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 ( 7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)
```

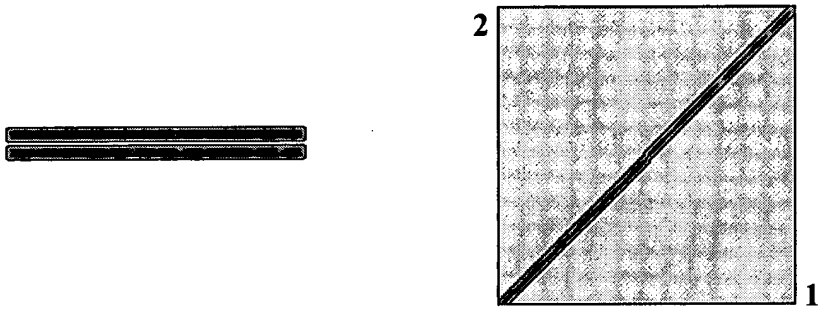
NCBI Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☑ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)

Sequence 2: gi|4507457|ref|NP_003225.1|transferrin receptor [Homo sapiens] >gi|37433|emb|CAA25527.1| unnamed protein product [Homo sapiens] >gi|339516|gb|AAA61153.1| transferrin receptor >gi|224192|prf||1011297A transferrin receptor
Length = 760 (1 .. 760)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

Score = 1529 bits (3958), Expect = 0.0
Identities = 759/760 (99%), Positives = 759/760 (99%), Gaps = 0/760 (0%)

SEQ ID NO 1 4

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            MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK
Sbjct  1    MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK  60

Query  61   RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR  120
            RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR
Sbjct  61   RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR  120

Query  121  RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK  180
            RLYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK
Sbjct  121  RLYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK  180

Query  181  VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK  240
```

```
            VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK
Sbjct  181  VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK  240

Query  241  KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH  300
            KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH
Sbjct  241  KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH  300

Query  301  AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD  360
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Sbjct  301  AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD  360

Query  361  STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG  420
            STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
Sbjct  361  STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG  420

Query  421  VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT  480
            VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
Sbjct  421  VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT  480

Query  481  YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA  540
            YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
Sbjct  481  YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA  540

Query  541  AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK  600
            AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
Sbjct  541  AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK  600

Query  601  LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF  660
            LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
Sbjct  601  LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF  660

Query  661  GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK  720
            GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
Sbjct  661  GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK  720

Query  721  QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  760
            QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct  721  QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  760



CPU time:     0.04 user secs.       0.01 sys. secs          0.05 total secs.

Lambda     K      H
   0.318    0.135    0.399

Gapped
Lambda     K      H
   0.267   0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 4451
Number of extensions: 2525
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
```

```
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 ( 7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)
```

Blast 2 Sequences results

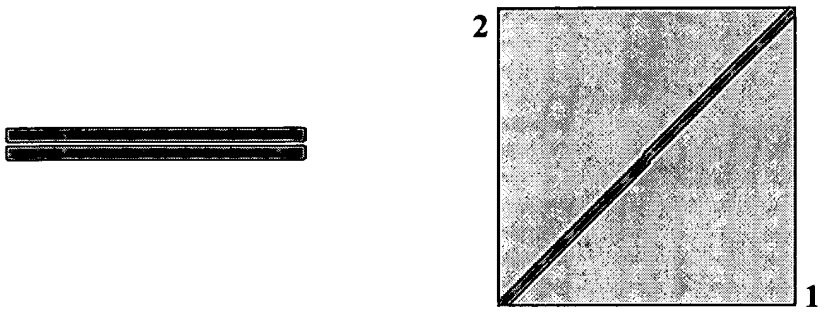
PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☑ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)

Sequence 2: gi|37433|emb|CAA25527.1|unnamed protein product [Homo sapiens] >gi|4507457|ref|NP_003225.1| transferrin receptor [Homo sapiens] >gi|339516|gb|AAA61153.1| transferrin receptor >gi|224192|prf||1011297A transferrin receptor
Length = 760 (1 .. 760)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

Score = 1529 bits (3958), Expect = 0.0
Identities = 759/760 (99%), Positives = 759/760 (99%), Gaps = 0/760 (0%)

SEQ ID NO: 1 5

```
Query  1    MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK  60
            MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK
Sbjct  1    MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK  60

Query  61   RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR  120
            RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR
Sbjct  61   RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR  120

Query  121  RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK  180
            RLYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK
Sbjct  121  RLYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK  180

Query  181  VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK  240
```

```
            VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK
Sbjct  181  VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK  240

Query  241  KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH  300
            KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH
Sbjct  241  KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH  300

Query  301  AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD  360
            AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD
Sbjct  301  AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD  360

Query  361  STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG  420
            STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
Sbjct  361  STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG  420

Query  421  VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT  480
            VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
Sbjct  421  VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT  480

Query  481  YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA  540
            YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
Sbjct  481  YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA  540

Query  541  AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK  600
            AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
Sbjct  541  AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK  600

Query  601  LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF  660
            LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
Sbjct  601  LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF  660

Query  661  GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK  720
            GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
Sbjct  661  GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK  720

Query  721  QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  760
            QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct  721  QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  760


CPU time:     0.03 user secs.       0.01 sys. secs          0.04 total secs.

Lambda     K      H
   0.318    0.135    0.399

Gapped
Lambda     K      H
   0.267   0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 4451
Number of extensions: 2525
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
```

```
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 ( 7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)
```

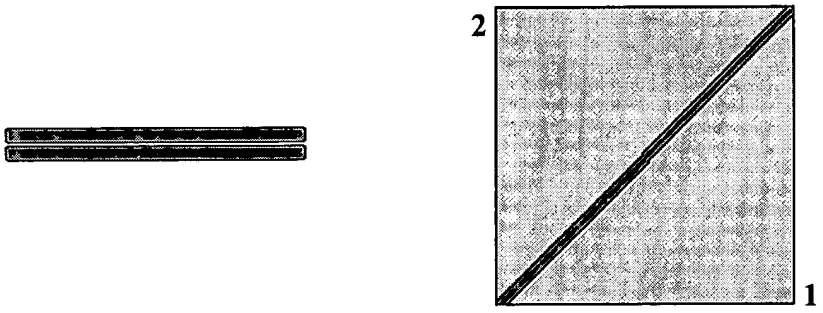
Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☑ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)

Sequence 2: gi|339516|gb|AAA61153.1|transferrin receptor >gi|4507457|ref|NP_003225.1| transferrin receptor [Homo sapiens] >gi|37433|emb|CAA25527.1| unnamed protein product [Homo sapiens] >gi|224192|prf||1011297A transferrin receptor
Length = 760 (1 .. 760)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

```
 Score = 1529 bits (3958),  Expect = 0.0
 Identities = 759/760 (99%), Positives = 759/760 (99%), Gaps = 0/760 (0%)

Query  1    MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK  60
            MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK
Sbjct  1    MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK  60

Query  61   RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR  120
            RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR
Sbjct  61   RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR  120

Query  121  RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK  180
            RLYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK
Sbjct  121  RLYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK  180

Query  181  VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK  240
```

```
            VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK
Sbjct  181  VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK  240

Query  241  KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH  300
            KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH
Sbjct  241  KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH  300

Query  301  AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD  360
            AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD
Sbjct  301  AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD  360

Query  361  STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG  420
            STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
Sbjct  361  STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG  420

Query  421  VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT  480
            VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
Sbjct  421  VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT  480

Query  481  YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA  540
            YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
Sbjct  481  YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA  540

Query  541  AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK  600
            AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
Sbjct  541  AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK  600

Query  601  LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF  660
            LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
Sbjct  601  LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF  660

Query  661  GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK  720
            GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
Sbjct  661  GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK  720

Query  721  QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  760
            QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct  721  QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  760


CPU time:     0.04 user secs.       0.00 sys. secs          0.04 total secs.

Lambda     K      H
   0.318    0.135    0.399

Gapped
Lambda     K      H
   0.267   0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 4451
Number of extensions: 2525
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
```

```
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 ( 7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)
```

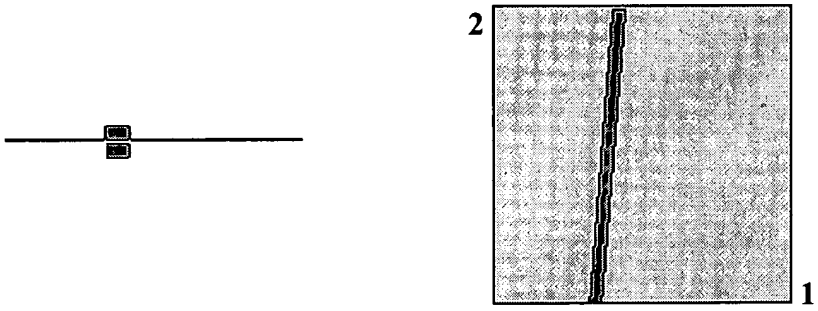
Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☑ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)

Sequence 2: gi|1336700|gb|AAB35972.1|transferrin receptor; TfR [Cavia] >gi|2144140|pir||S68317 transferrin receptor - guinea pig (fragment)
Length = 63 (1 .. 63)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

Score = 118 bits (295), Expect = 2e-24
Identities = 54/63 (85%), Positives = 57/63 (90%), Gaps = 0/63 (0%)

SEQ ID NO 1 7

```
Query  261  KITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHAHLGTGDPYTPGFPSFNHTQ  320
            KITFAEKVANAESLNA+GVLIY+D TKFPI  A+L  FGH HLGTGDPYTPGFPSFNHTQ
Sbjct  1    KITFAEKVANAESLNALGVLIYLDWTKFPIPKADLPVFGHVHLGTGDPYTPGFPSFNHTQ  60

Query  321  FPP  323
            FPP
Sbjct  61   FPP  63
```

```
CPU time:      0.03 user secs.       0.01 sys. secs          0.04 total secs.

Lambda     K      H
```

```
   0.318    0.135    0.399

Gapped
Lambda      K       H
   0.267   0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 413
Number of extensions: 242
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 ( 7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)
```

Blast 2 Sequences results

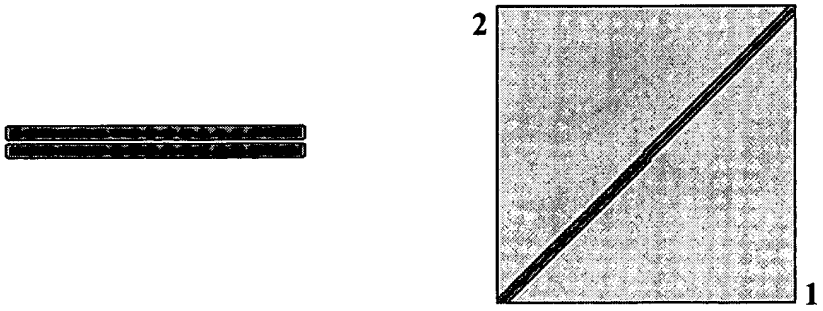
PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☑ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)

Sequence 2: gi|108935939|sp|P02786|TFR1_HUMANTransferrin receptor protein 1 (TfR1) (TR) (TfR) (Trfr) (CD71 antigen) (T9) (p90) >gi|6164848|gb|AAF04564.1|AF187320_1 transferrin receptor [Homo sapiens] >gi|12654697|gb|AAH01188.1| TFRC protein [Homo sapiens] >gi|94717625|gb|ABF47088.1| transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

Score = 1531 bits (3964), Expect = 0.0
Identities = 760/760 (100%), Positives = 760/760 (100%), Gaps = 0/760 (0%)

SEQ ID NO 1 8

```
Query  1    MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK  60
            MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK
Sbjct  1    MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK  60

Query  61   RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR  120
            RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR
Sbjct  61   RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR  120

Query  121  RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK  180
            RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK
Sbjct  121  RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK  180
```

```
Query  181  VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK  240
            VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK
Sbjct  181  VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK  240

Query  241  KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH  300
            KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH
Sbjct  241  KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH  300

Query  301  AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAAEKLFGNMEGDCPSDWKTD  360
            AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAAEKLFGNMEGDCPSDWKTD
Sbjct  301  AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAAEKLFGNMEGDCPSDWKTD  360

Query  361  STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG  420
            STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
Sbjct  361  STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG  420

Query  421  VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT  480
            VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
Sbjct  421  VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT  480

Query  481  YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA  540
            YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
Sbjct  481  YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA  540

Query  541  AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK  600
            AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
Sbjct  541  AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK  600

Query  601  LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF  660
            LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
Sbjct  601  LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF  660

Query  661  GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK  720
            GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
Sbjct  661  GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK  720

Query  721  QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  760
            QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct  721  QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  760


CPU time:     0.04 user secs.       0.01 sys. secs          0.05 total secs.

Lambda     K      H
   0.318    0.135    0.399

Gapped
Lambda     K      H
   0.267   0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 4468
Number of extensions: 2537
Number of successful extensions: 1
Number of sequences better than 10.0: 1
```

```
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 ( 7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)
```

Blast 2 Sequences results

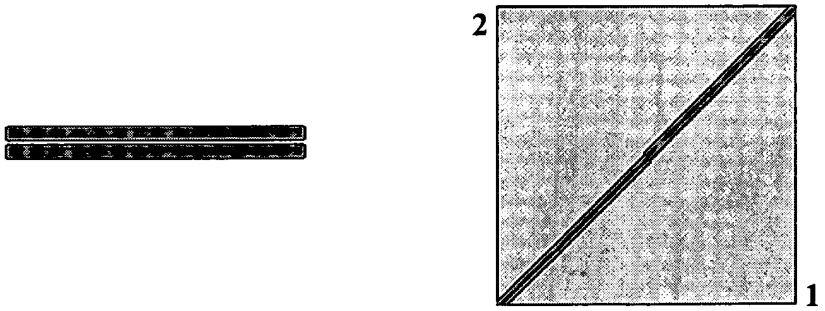
PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☑ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: lcl|1_seq_1
Length = 2249 (1 .. 2249)

Sequence 2: lcl|2_seq_2
Length = 2249 (1 .. 2249)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

Score = 3152 bits (8171), Expect = 0.0
Identities = 2246/2249 (99%), Positives = 2246/2249 (99%), Gaps = 0/2249 (0%)

SEQ ID NO 1 / 9

```
Query  1     METMETASPGLNALAARGSERALAPHESERASNLEUPHEXXXXXXXXXPRLEUSERTYRT  60
             METMETASPGLNALAARGSERALAPHESERASNLEUPHEGLYGLYGLUPRLEUSERTYRT
Sbjct  1     METMETASPGLNALAARGSERALAPHESERASNLEUPHEGLYGLYGLUPRLEUSERTYRT  60

Query  61    HRARGPHESERLEUALAARGGLNVALASPGLYASPASNSERHISVALGLUMETXXXXXXX  120
             HRARGPHESERLEUALAARGGLNVALASPGLYASPASNSERHISVALGLUMETLYSLEUA
Sbjct  61    HRARGPHESERLEUALAARGGLNVALASPGLYASPASNSERHISVALGLUMETLYSLEUA  120

Query  121   XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTHRLYSALAASNVALTHRLYSPRLYSAR  180
             LAVALASPGLUGLUGLUASNALAASPASNASNTHRLYSALAASNVALTHRLYSPRLYSAR
Sbjct  121   LAVALASPGLUGLUGLUASNALAASPASNASNTHRLYSALAASNVALTHRLYSPRLYSAR  180

Query  181   GCYSSERGLYSERILECYSTYRGLYTHRXXXXXXXXXXXXXXXXXXXXXXXXXXXXYPH  240
             GCYSSERGLYSERILECYSTYRGLYTHRILEALAVALILEVALPHEPHELEUILEGLYPH
Sbjct  181   GCYSSERGLYSERILECYSTYRGLYTHRILEALAVALILEVALPHEPHELEUILEGLYPH  240
```

```
Query  241   EMETILEGLYTYRLEUGLYTYRCYSLYSGLYVALGLUPRLYSTHRGLUCYSXXXXXXXXX  300
             EMETILEGLYTYRLEUGLYTYRCYSLYSGLYVALGLUPRLYSTHRGLUCYSGLUARGLEU
Sbjct  241   EMETILEGLYTYRLEUGLYTYRCYSLYSGLYVALGLUPRLYSTHRGLUCYSGLUARGLEU  300

Query  301   XXXXXYTHRGLUSEXXXXXXXXXXXXXXXXXXXXXXXUASPPHEPXXXXXXXXXXXXXXEU  360
             ALAGLYTHRGLUSERPRVALARGGLUGLUPRGLYGLUASPPHEPRALAALAARGARGLEU
Sbjct  301   ALAGLYTHRGLUSERPRVALARGGLUGLUPRGLYGLUASPPHEPRALAALAARGARGLEU  360

Query  361   TYRTRPASPASPLEULYSARGLYSLEUSERGLULYSLEUASPSERTHRASPPHETHRGLY  420
             TYRTRPASPASPLEULYSARGLYSLEUSERGLULYSLEUASPSERTHRASPPHETHR
Sbjct  361   TYRTRPASPASPLEULYSARGLYSLEUSERGLULYSLEUASPSERTHRASPPHETHRSER  420

Query  421   THRIXXXXXXXXXXXASNGLUASNSERTYXXXXXXXXXXXXXXXXXYSERGLNLYSASPG  480
             THRILELYSLEULEUASNGLUASNSERTYRVALPRARGGLUALAGLYSERGLNLYSASPG
Sbjct  421   THRILELYSLEULEUASNGLUASNSERTYRVALPRARGGLUALAGLYSERGLNLYSASPG  480

Query  481   LUASNXXXXXXXXXTYRVALGLUASNGLNPHEARGGLUPHELYSLEUSERLYSVALTRPA  540
             LUASNLEUALALEUTYRVALGLUASNGLNPHEARGGLUPHELYSLEUSERLYSVALTRPA
Sbjct  481   LUASNLEUALALEUTYRVALGLUASNGLNPHEARGGLUPHELYSLEUSERLYSVALTRPA  540

Query  541   RGASPGLNHISPHEVALLYSILEGLNVALLYSASPSERALAGLNASNSERXXXXXXXXXX  600
             RGASPGLNHISPHEVALLYSILEGLNVALLYSASPSERALAGLNASNSERVALILEILEV
Sbjct  541   RGASPGLNHISPHEVALLYSILEGLNVALLYSASPSERALAGLNASNSERVALILEILEV  600

Query  601   XXXSPLYSASNGLYARGLEUVALTYRLEUVALGLUASNPRGLYGLYTYRVALALATYRSE  660
             ALASPLYSASNGLYARGLEUVALTYRLEUVALGLUASNPRGLYGLYTYRVALALATYRSE
Sbjct  601   ALASPLYSASNGLYARGLEUVALTYRLEUVALGLUASNPRGLYGLYTYRVALALATYRSE  660

Query  661   RLYSALAALATHRVALTHRGLYLYSLEUVALHISALAASNPHEGLYTHRLYSLYSASPPH  720
             RLYSALAALATHRVALTHRGLYLYSLEUVALHISALAASNPHEGLYTHRLYSLYSASPPH
Sbjct  661   RLYSALAALATHRVALTHRGLYLYSLEUVALHISALAASNPHEGLYTHRLYSLYSASPPH  720

Query  721   EGLUASPLEUTYRTHRPRVALASNGLYSERXXXXXXXXXXXXXXXXXXXXXSILETHR  780
             EGLUASPLEUTYRTHRPRVALASNGLYSERILEVALILEVALARGALAGLYLYSILETHR
Sbjct  721   EGLUASPLEUTYRTHRPRVALASNGLYSERILEVALILEVALARGALAGLYLYSILETHR  780

Query  781   PHEXXXXXXXXXXXXXXXXXXXXXXXERLEUASNALAILEGLYVALLEUILETYRMET  840
             PHEALAGLULYSVALALAASNALAGLUSERLEUASNALAILEGLYVALLEUILETYRMET
Sbjct  781   PHEALAGLULYSVALALAASNALAGLUSERLEUASNALAILEGLYVALLEUILETYRMET  840

Query  841   ASPGLNTHRLYSPHEPRILEVXXXXXXXXXXXXEUSERPHEPHEGLYHISALAHISLEUG  900
             ASPGLNTHRLYSPHEPRILEVALASNALAGLULEUSERPHEPHEGLYHISALAHISLEUG
Sbjct  841   ASPGLNTHRLYSPHEPRILEVALASNALAGLULEUSERPHEPHEGLYHISALAHISLEUG  900

Query  901   LYTHRGLYASPPRTYRTHRPRGLYPHEPRSERPHEASNHISTHRGLNPHXXXXXXXXXXX  960
             LYTHRGLYASPPRTYRTHRPRGLYPHEPRSERPHEASNHISTHRGLNPHEPRPRSERARG
Sbjct  901   LYTHRGLYASPPRTYRTHRPRGLYPHEPRSERPHEASNHISTHRGLNPHEPRPRSERARG  960

Query  961   XXXXXXXLYLEUPRASNILEPRVALGLNTHRILESEXXXXXXXXXXXXXXXXXYSLEUPH  1020
             SERSERGLYLEUPRASNILEPRVALGLNTHRILESERARGALAALAALAGLULYSLEUPH
Sbjct  961   SERSERGLYLEUPRASNILEPRVALGLNTHRILESERARGALAALAALAGLULYSLEUPH  1020

Query  1021  EGLYASNMETGLUGLYASPCYSPRSERASPTRPLYSTHRASPSERTHRCYSARGMETVAL  1080
             EGLYASNMETGLUGLYASPCYSPRSERASPTRPLYSTHRASPSERTHRCYSARGMETVAL
Sbjct  1021  EGLYASNMETGLUGLYASPCYSPRSERASPTRPLYSTHRASPSERTHRCYSARGMETVAL  1080

Query  1081  THRSERGLUSERLYSASNVALLYSLEUTHRVALSERASNVAXXXXXXXXXXXXXXXXXX  1140
             THRSERGLUSERLYSASNVALLYSLEUTHRVALSERASNVALLEULYSGLUILELYSILE
Sbjct  1081  THRSERGLUSERLYSASNVALLYSLEUTHRVALSERASNVALLEULYSGLUILELYSILE  1140
```

```
Query  1141  XXUASNILEPHEGLYVALILELYSGLYPHEVALGLUPRASPHISTYRXXXXXXXXXXXXX  1200
             LEUASNILEPHEGLYVALILELYSGLYPHEVALGLUPRASPHISTYRVALVALVALGLYA
Sbjct  1141  LEUASNILEPHEGLYVALILELYSGLYPHEVALGLUPRASPHISTYRVALVALVALGLYA  1200

Query  1201  XXXXXXXXXSPALATRPGLYPRGXXXXXXXXXXSSERGLYVALGLYTHRXXXXXXXXXXX  1260
             LAGLNARGASPALATRPGLYPRGLYALAALALYSSERGLYVALGLYTHRALALEULEULE
Sbjct  1201  LAGLNARGASPALATRPGLYPRGLYALAALALYSSERGLYVALGLYTHRALALEULEULE  1260

Query  1261  XXXXXXXXXXXXNMETPHESERASPMETVALLEULYSASPGLYPHEGLNPRSERARGSER  1320
             ULYSLEUALAGLNMETPHESERASPMETVALLEULYSASPGLYPHEGLNPRSERARGSER
Sbjct  1261  ULYSLEUALAGLNMETPHESERASPMETVALLEULYSASPGLYPHEGLNPRSERARGSER  1320

Query  1321  ILEILEPHEALASERTRPSERALAGLYASPPHEGLYSERVALGLYALATHRGLUTRPLEU  1380
             ILEILEPHEALASERTRPSERALAGLYASPPHEGLYSERVALGLYALATHRGLUTRPLEU
Sbjct  1321  ILEILEPHEALASERTRPSERALAGLYASPPHEGLYSERVALGLYALATHRGLUTRPLEU  1380

Query  1381  GLUGLYTYXXXXXXXXXXXXXXXXXXXXYSALAPHETHRTYRILEASNLEUASPLYSALA  1440
             GLUGLYTYRLEUSERSERLEUHISLEULYSALAPHETHRTYRILEASNLEUASPLYSALA
Sbjct  1381  GLUGLYTYRLEUSERSERLEUHISLEULYSALAPHETHRTYRILEASNLEUASPLYSALA  1440

Query  1441  VALLEUGLYTHRSERASNPHELYSVALSERALASERPRLEULEUTYRTHRLEUILEGLUL  1500
             VALLEUGLYTHRSERASNPHELYSVALSERALASERPRLEULEUTYRTHRLEUILEGLUL
Sbjct  1441  VALLEUGLYTHRSERASNPHELYSVALSERALASERPRLEULEUTYRTHRLEUILEGLUL  1500

Query  1501  YSTHRMETGLNASNVALLYSHISPRVALTHRGLYGLNPHELEUTYRGLNASPSERASNTR  1560
             YSTHRMETGLNASNVALLYSHISPRVALTHRGLYGLNPHELEUTYRGLNASPSERASNTR
Sbjct  1501  YSTHRMETGLNASNVALLYSHISPRVALTHRGLYGLNPHELEUTYRGLNASPSERASNTR  1560

Query  1561  PALASERLYSVALGLULYSLEUTHRLEXXXXXXXXXXXXXXHEPRPHELEUALATYRSER  1620
             PALASERLYSVALGLULYSLEUTHRLEUASPASNALAALAPHEPRPHELEUALATYRSER
Sbjct  1561  PALASERLYSVALGLULYSLEUTHRLEUASPASNALAALAPHEPRPHELEUALATYRSER  1620

Query  1621  GLYILEPRALAVALSERPHECYSPHECYSGLUASPTHRASPTYRPRTYRLEUGLYTHRTH  1680
             GLYILEPRALAVALSERPHECYSPHECYSGLUASPTHRASPTYRPRTYRLEUGLYTHRTH
Sbjct  1621  GLYILEPRALAVALSERPHECYSPHECYSGLUASPTHRASPTYRPRTYRLEUGLYTHRTH  1680

Query  1681  RMETASPTHRTYRLYSXXXXXXXXXXXUARGILEPRGLULEUASNLYSVXXXXXXXXXXX  1740
             RMETASPTHRTYRLYSGLULEUILEGLUARGILEPRGLULEUASNLYSVALALAARGALA
Sbjct  1681  RMETASPTHRTYRLYSGLULEUILEGLUARGILEPRGLULEUASNLYSVALALAARGALA  1740

Query  1741  XXXXXXXXXXXXXXXXXXXXNPHEVALILELYSLEUTHRHISASPVALGLULEUASNLEU  1800
             ALAALAGLUVALALAGLYGLNPHEVALILELYSLEUTHRHISASPVALGLULEUASNLEU
Sbjct  1741  ALAALAGLUVALALAGLYGLNPHEVALILELYSLEUTHRHISASPVALGLULEUASNLEU  1800

Query  1801  ASPTYRGLUARGTYRASNSERGLNLEULEUSERPHEVALARGASPLEUASNGLNTYRARG  1860
             ASPTYRGLUARGTYRASNSERGLNLEULEUSERPHEVALARGASPLEUASNGLNTYRARG
Sbjct  1801  ASPTYRGLUARGTYRASNSERGLNLEULEUSERPHEVALARGASPLEUASNGLNTYRARG  1860

Query  1861  ALAASPILELYSGLUMETGLYLEUSERLEUGLNTRPLEUTYRSERALAARGGLYASPPHE  1920
             ALAASPILELYSGLUMETGLYLEUSERLEUGLNTRPLEUTYRSERALAARGGLYASPPHE
Sbjct  1861  ALAASPILELYSGLUMETGLYLEUSERLEUGLNTRPLEUTYRSERALAARGGLYASPPHE  1920

Query  1921  PHEARGALATHRSERARGLEUTHRTHRASPPHEGLYASNALAGLULYSTHRASPARGPHE  1980
             PHEARGALATHRSERARGLEUTHRTHRASPPHEGLYASNALAGLULYSTHRASPARGPHE
Sbjct  1921  PHEARGALATHRSERARGLEUTHRTHRASPPHEGLYASNALAGLULYSTHRASPARGPHE  1980

Query  1981  VALMETLYSLYSLEUASNASPARGVALMETARGVALGLUTYRHISPHELEUSERPRTYRV  2040
             VALMETLYSLYSLEUASNASPARGVALMETARGVALGLUTYRHISPHELEUSERPRTYRV
Sbjct  1981  VALMETLYSLYSLEUASNASPARGVALMETARGVALGLUTYRHISPHELEUSERPRTYRV  2040
```

```
Query  2041  ALSERPRLYSGLUSERPRPHEARGHISVALPHETRPGLYSERGLYSERHISTHXXXXXXX  2100
             ALSERPRLYSGLUSERPRPHEARGHISVALPHETRPGLYSERGLYSERHISTHRLEUPRA
Sbjct  2041  ALSERPRLYSGLUSERPRPHEARGHISVALPHETRPGLYSERGLYSERHISTHRLEUPRA  2100

Query  2101  XXXXXXXXGLUASNLEULYSLEUARGLYSGLNASNASNGLYALAPHEASNGLUTHRLEUP  2160
             LALEULEUGLUASNLEULYSLEUARGLYSGLNASNASNGLYALAPHEASNGLUTHRLEUP
Sbjct  2101  LALEULEUGLUASNLEULYSLEUARGLYSGLNASNASNGLYALAPHEASNGLUTHRLEUP  2160

Query  2161  HEARGASNGLNXXXXXXXXXXXXTHRTRPTHRIXXXXXXXXXXXXXXXXXXXXXXXERG  2220
             HEARGASNGLNLEUALALEUALATHRTRPTHRILEGLNGLYALAALAASNALALEUSERG
Sbjct  2161  HEARGASNGLNLEUALALEUALATHRTRPTHRILEGLNGLYALAALAASNALALEUSERG  2220

Query  2221  LYASPVALTRPASPILEASPASNGLUPHE  2249
             LYASPVALTRPASPILEASPASNGLUPHE
Sbjct  2221  LYASPVALTRPASPILEASPASNGLUPHE  2249
```

```
CPU time:     0.05 user secs.       0.01 sys. secs          0.06 total secs.

Lambda     K      H
   0.314    0.130    0.376

Gapped
Lambda     K      H
   0.267   0.0410    0.140
```

```
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 94,211
Number of extensions: 37877
Number of successful extensions: 747
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 2249
Length of database: 1,435,209,301
Length adjustment: 151
Effective length of query: 2098
Effective length of database: 1,435,209,150
Effective search space: 3011068796700
Effective search space used: 3011068796700
Neighboring words threshold: 9
X1: 16 ( 7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 42 (22.0 bits)
S2: 88 (38.5 bits)
```

NCBI Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☑ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)

Sequence 2: lcl|seq_2
Length = 760 (1 .. 760)

NOTE:Bitscore and expect value are calculated based on the size of the nr database.

Score = 1529 bits (3958), Expect = 0.0
Identities = 759/760 (99%), Positives = 759/760 (99%), Gaps = 0/760 (0%)

SEQIDNO

```
1     Query  1    MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK  60
             MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK
10    Sbjct  1    MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDEEENADNNTKANVTKPK  60

      Query  61   RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR  120
             RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR
      Sbjct  61   RCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAAR  120

      Query  121  RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK  180
             RLYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK
      Sbjct  121  RLYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK  180

      Query  181  VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK  240
             VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK
      Sbjct  181  VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK  240
```

```
Query  241  KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH  300
            KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH
Sbjct  241  KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH  300

Query  301  AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD  360
            AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD
Sbjct  301  AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD  360

Query  361  STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG  420
            STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
Sbjct  361  STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG  420

Query  421  VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT  480
            VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
Sbjct  421  VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT  480

Query  481  YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA  540
            YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
Sbjct  481  YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA  540

Query  541  AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK  600
            AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
Sbjct  541  AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK  600

Query  601  LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF  660
            LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
Sbjct  601  LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF  660

Query  661  GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK  720
            GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
Sbjct  661  GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK  720

Query  721  QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  760
            QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct  721  QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  760


CPU time:     0.03 user secs.       0.00 sys. secs          0.03 total secs.

Lambda     K      H
   0.318    0.135    0.399

Gapped
Lambda     K      H
   0.267   0.0410    0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 4451
Number of extensions: 2525
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
```

```
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 ( 7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)
```

Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ☑ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)

Sequence 2: lcl|seq_2
Length = 640 (1 .. 640)

NOTE:Bitscore and expect value are calculated based on the size of the nr database.

Score = 1286 bits (3327), Expect = 0.0
Identities = 639/640 (99%), Positives = 639/640 (99%), Gaps = 0/640 (0%)

SEQ ID NO 1

```
Query  121  RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK  180
            RLYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK
Sbjct  1    RLYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK  60

Query  181  VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK  240
            VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK
Sbjct  61   VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK  120

Query  241  KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH  300
            KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH
Sbjct  121  KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH  180

Query  301  AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD  360
            AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD
Sbjct  181  AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD  240
```

```
Query  361  STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG  420
            STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
Sbjct  241  STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG  300

Query  421  VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT  480
            VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
Sbjct  301  VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT  360

Query  481  YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA  540
            YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
Sbjct  361  YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA  420

Query  541  AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK  600
            AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
Sbjct  421  AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK  480

Query  601  LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF  660
            LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
Sbjct  481  LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF  540

Query  661  GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK  720
            GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
Sbjct  541  GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK  600

Query  721  QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  760
            QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct  601  QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  640


CPU time:     0.03 user secs.       0.00 sys. secs          0.03 total secs.

Lambda     K      H
   0.318    0.135    0.399

Gapped
Lambda     K      H
   0.267   0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 3743
Number of extensions: 2118
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 ( 7.3 bits)
X2: 38 (14.6 bits)
```

```
X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)
```

Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ☑ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)

Sequence 2: lcl|seq_2
Length = 640 (1 .. 640)

NOTE:Bitscore and expect value are calculated based on the size of the nr database.

Score = 1286 bits (3327), Expect = 0.0
Identities = 639/640 (99%), Positives = 639/640 (99%), Gaps = 0/640 (0%)

SEQIDNO

```
1   Query  121  RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK  180
               RLYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK
12  Sbjct  1    RLYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK  60

    Query  181  VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK  240
               VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK
    Sbjct  61   VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK  120

    Query  241  KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH  300
               KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH
    Sbjct  121  KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH  180

    Query  301  AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD  360
               AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD
    Sbjct  181  AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD  240
```

```
Query  361  STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG  420
            STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
Sbjct  241  STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG  300

Query  421  VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT  480
            VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
Sbjct  301  VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT  360

Query  481  YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA  540
            YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
Sbjct  361  YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA  420

Query  541  AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK  600
            AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
Sbjct  421  AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK  480

Query  601  LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF  660
            LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
Sbjct  481  LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF  540

Query  661  GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK  720
            GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
Sbjct  541  GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK  600

Query  721  QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  760
            QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct  601  QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  640


CPU time:     0.03 user secs.       0.01 sys. secs          0.04 total secs.

Lambda     K      H
   0.318    0.135    0.399

Gapped
Lambda     K      H
   0.267   0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 3743
Number of extensions: 2118
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 ( 7.3 bits)
X2: 38 (14.6 bits)
```

```
X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)
```

Blast 2 Sequences results

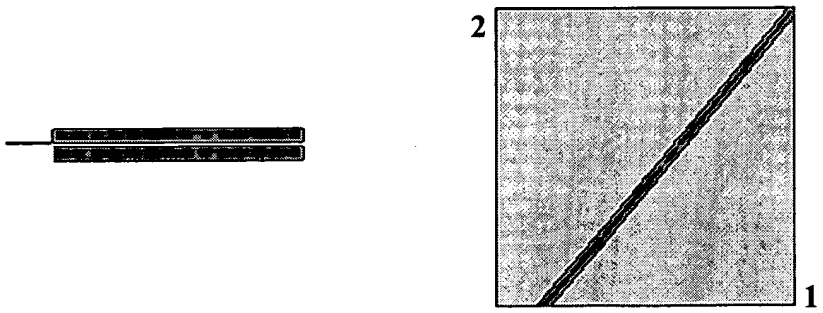
PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ☑ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)

Sequence 2: lcl|seq_2
Length = 640 (1 .. 640)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

Score = 1286 bits (3327), Expect = 0.0
Identities = 639/640 (99%), Positives = 639/640 (99%), Gaps = 0/640 (0%)

SEQIDNO

```
1    Query  121  RLYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK  180
             RLYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK
13   Sbjct  1    RLYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK  60

     Query  181  VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK  240
             VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK
     Sbjct  61   VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK  120

     Query  241  KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH  300
             KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH
     Sbjct  121  KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH  180

     Query  301  AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD  360
             AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD
     Sbjct  181  AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD  240
```

```
Query  361  STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG  420
            STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
Sbjct  241  STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG  300

Query  421  VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT  480
            VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT
Sbjct  301  VGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFT  360

Query  481  YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA  540
            YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
Sbjct  361  YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA  420

Query  541  AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK  600
            AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
Sbjct  421  AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK  480

Query  601  LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF  660
            LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
Sbjct  481  LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF  540

Query  661  GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK  720
            GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK
Sbjct  541  GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRK  600

Query  721  QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  760
            QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct  601  QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  640


CPU time:     0.03 user secs.       0.01 sys. secs          0.04 total secs.

Lambda     K      H
   0.318    0.135    0.399

Gapped
Lambda     K      H
   0.267   0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 3743
Number of extensions: 2118
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 ( 7.3 bits)
X2: 38 (14.6 bits)
```

```
X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)
```

Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ☑ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)

Sequence 2: lcl|seq_2
Length = 639 (1 .. 639)

NOTE:Bitscore and expect value are calculated based on the size of the nr database.

Score = 1281 bits (3314), Expect = 0.0
Identities = 636/639 (99%), Positives = 637/639 (99%), Gaps = 0/639 (0%)

SEQIDNO

```
1   Query  122  LYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSKV  181
            LYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVEN+FREFKLSKV
14  Sbjct  1    LYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENEFREFKLSKV  60

    Query  182  WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK  241
            WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK
    Sbjct  61   WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK  120

    Query  242  DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA  301
            DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA
    Sbjct  121  DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA  180

    Query  302  HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS  361
            HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS
    Sbjct  181  HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS  240
```

```
Query  362  TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV  421
            TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
Sbjct  241  TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV  300

Query  422  GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY  481
            GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
Sbjct  301  GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY  360

Query  482  INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA  541
            INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA
Sbjct  361  INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA  420

Query  542  FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL  601
            FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
Sbjct  421  FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL  480

Query  602  THDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG  661
            THDVELNLDYE YNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
Sbjct  481  THDVELNLDYEEYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG  540

Query  662  NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ  721
            NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ
Sbjct  541  NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ  600

Query  722  NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  760
            NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct  601  NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  639


CPU time:     0.03 user secs.       0.01 sys. secs          0.04 total secs.

Lambda     K      H
   0.318    0.135    0.399

Gapped
Lambda     K      H
   0.267   0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 3738
Number of extensions: 2121
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 ( 7.3 bits)
X2: 38 (14.6 bits)
```

```
X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)
```

Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

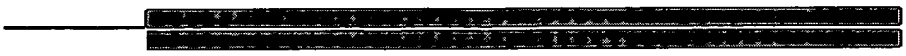
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ☑ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)

Sequence 2: lcl|seq_2
Length = 639 (1 .. 639)

NOTE:Bitscore and expect value are calculated based on the size of the nr database.



```
 Score = 1281 bits (3314),  Expect = 0.0
 Identities = 636/639 (99%), Positives = 637/639 (99%), Gaps = 0/639 (0%)

Query  122  LYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSKV  181
            LYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVEN+FREFKLSKV
Sbjct  1    LYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENEFREFKLSKV  60

Query  182  WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK  241
            WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK
Sbjct  61   WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK  120

Query  242  DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA  301
            DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA
Sbjct  121  DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA  180

Query  302  HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS  361
            HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS
Sbjct  181  HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS  240
```

SEQ ID NO 1 15

```
Query  362  TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV  421
            TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
Sbjct  241  TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV  300

Query  422  GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY  481
            GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
Sbjct  301  GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY  360

Query  482  INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA  541
            INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA
Sbjct  361  INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA  420

Query  542  FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL  601
            FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
Sbjct  421  FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL  480

Query  602  THDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG  661
            THDVELNLDYE YNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
Sbjct  481  THDVELNLDYEEYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG  540

Query  662  NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ  721
            NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ
Sbjct  541  NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ  600

Query  722  NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  760
            NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct  601  NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  639


CPU time:     0.04 user secs.       0.01 sys. secs          0.05 total secs.

Lambda     K      H
   0.318    0.135    0.399

Gapped
Lambda     K      H
   0.267   0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 3738
Number of extensions: 2121
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 ( 7.3 bits)
X2: 38 (14.6 bits)
```

X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)

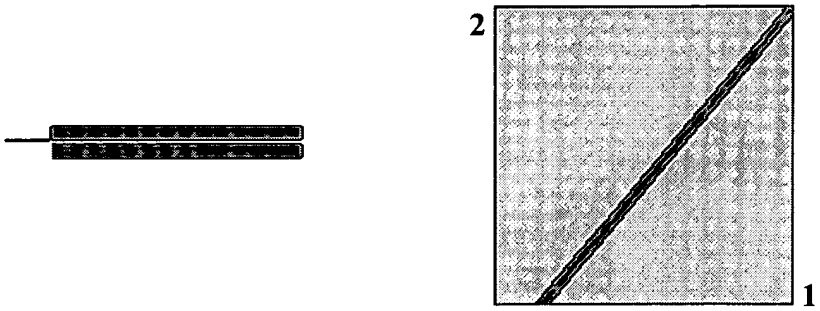
NCBI Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ☑ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)

Sequence 2: lcl|seq_2
Length = 639 (1 .. 639)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

Score = 1281 bits (3314), Expect = 0.0
SEQIDNO Identities = 636/639 (99%), Positives = 637/639 (99%), Gaps = 0/639 (0%)

```
1    Query  122  LYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSKV  181
             LYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVEN+FREFKLSKV
16   Sbjct  1    LYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENEFREFKLSKV  60

     Query  182  WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK  241
             WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK
     Sbjct  61   WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK  120

     Query  242  DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA  301
             DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA
     Sbjct  121  DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA  180

     Query  302  HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS  361
             HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS
     Sbjct  181  HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS  240
```

```
Query  362  TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV  421
            TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
Sbjct  241  TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV  300

Query  422  GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY  481
            GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
Sbjct  301  GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY  360

Query  482  INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA  541
            INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA
Sbjct  361  INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA  420

Query  542  FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL  601
            FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
Sbjct  421  FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL  480

Query  602  THDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG  661
            THDVELNLDYE YNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
Sbjct  481  THDVELNLDYEEYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG  540

Query  662  NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ  721
            NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ
Sbjct  541  NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ  600

Query  722  NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  760
            NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct  601  NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  639


CPU time:     0.04 user secs.       0.00 sys. secs          0.04 total secs.

Lambda     K      H
   0.318    0.135    0.399

Gapped
Lambda     K      H
   0.267   0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 3738
Number of extensions: 2121
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 ( 7.3 bits)
X2: 38 (14.6 bits)
```

```
X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)
```

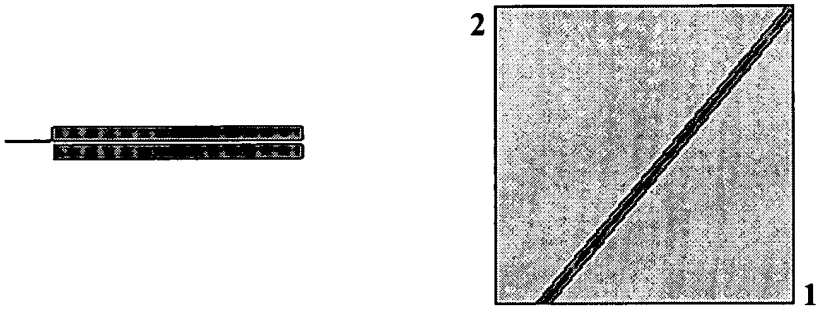
Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ☑ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)

Sequence 2: lcl|seq_2
Length = 639 (1 .. 639)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

Score = 1281 bits (3314), Expect = 0.0
Identities = 636/639 (99%), Positives = 637/639 (99%), Gaps = 0/639 (0%)

SEQ ID NO 1 / 17

```
Query  122  LYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSKV  181
            LYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVEN+FREFKLSKV
Sbjct  1    LYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENEFREFKLSKV  60

Query  182  WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK  241
            WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK
Sbjct  61   WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK  120

Query  242  DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA  301
            DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA
Sbjct  121  DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA  180

Query  302  HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS  361
            HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS
Sbjct  181  HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS  240
```

```
Query  362  TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV  421
            TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
Sbjct  241  TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV  300

Query  422  GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY  481
            GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
Sbjct  301  GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY  360

Query  482  INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA  541
            INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA
Sbjct  361  INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA  420

Query  542  FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL  601
            FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
Sbjct  421  FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL  480

Query  602  THDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG  661
            THDVELNLDYE YNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
Sbjct  481  THDVELNLDYEEYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG  540

Query  662  NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ  721
            NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ
Sbjct  541  NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ  600

Query  722  NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  760
            NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct  601  NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  639


CPU time:     0.03 user secs.       0.00 sys. secs          0.03 total secs.

Lambda     K      H
   0.318    0.135    0.399

Gapped
Lambda     K      H
   0.267   0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 3738
Number of extensions: 2121
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 ( 7.3 bits)
X2: 38 (14.6 bits)
```

```
X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)
```

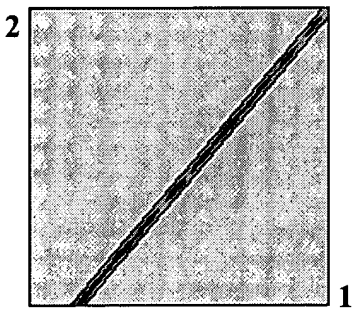
NCBI Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ☑ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)

Sequence 2: lcl|seq_2
Length = 639 (1 .. 639)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

```
 Score = 1281 bits (3314),  Expect = 0.0
 Identities = 636/639 (99%), Positives = 637/639 (99%), Gaps = 0/639 (0%)

Query  122  LYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSKV  181
            LYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVEN+FREFKLSKV
Sbjct  1    LYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENEFREFKLSKV  60

Query  182  WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK  241
            WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK
Sbjct  61   WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK  120

Query  242  DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA  301
            DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA
Sbjct  121  DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA  180

Query  302  HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS  361
            HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS
Sbjct  181  HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS  240
```

```
Query  362  TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV  421
            TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
Sbjct  241  TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV  300

Query  422  GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY  481
            GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
Sbjct  301  GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY  360

Query  482  INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA  541
            INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA
Sbjct  361  INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA  420

Query  542  FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL  601
            FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
Sbjct  421  FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL  480

Query  602  THDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG  661
            THDVELNLDYE YNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
Sbjct  481  THDVELNLDYEEYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG  540

Query  662  NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ  721
            NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ
Sbjct  541  NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ  600

Query  722  NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  760
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Sbjct  601  NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  639


CPU time:     0.03 user secs.       0.00 sys. secs          0.03 total secs.

Lambda     K      H
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Gapped
Lambda     K      H
   0.267   0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
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X1: 16 ( 7.3 bits)
X2: 38 (14.6 bits)
```

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X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)
```

Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ☑ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)

Sequence 2: lcl|seq_2
Length = 639 (1 .. 639)

NOTE:Bitscore and expect value are calculated based on the size of the nr database.

```
 Score = 1281 bits (3314),  Expect = 0.0
 Identities = 636/639 (99%), Positives = 637/639 (99%), Gaps = 0/639 (0%)

Query  122  LYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSKV  181
            LYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVEN+FREFKLSKV
Sbjct  1    LYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENEFREFKLSKV  60

Query  182  WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK  241
            WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK
Sbjct  61   WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK  120

Query  242  DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA  301
            DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA
Sbjct  121  DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA  180

Query  302  HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS  361
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Sbjct  181  HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS  240
```

SEQIDNO 1 (9

```
Query  362  TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV  421
            TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
Sbjct  241  TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV  300

Query  422  GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY  481
            GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
Sbjct  301  GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY  360

Query  482  INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA  541
            INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA
Sbjct  361  INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA  420

Query  542  FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL  601
            FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
Sbjct  421  FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL  480

Query  602  THDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG  661
            THDVELNLDYE YNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
Sbjct  481  THDVELNLDYEEYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG  540

Query  662  NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ  721
            NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ
Sbjct  541  NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ  600

Query  722  NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  760
            NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct  601  NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  639


CPU time:     0.04 user secs.       0.01 sys. secs          0.05 total secs.

Lambda     K      H
   0.318    0.135    0.399

Gapped
Lambda     K      H
   0.267   0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 3738
Number of extensions: 2121
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 ( 7.3 bits)
X2: 38 (14.6 bits)
```

```
X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)
```

Blast 2 Sequences results

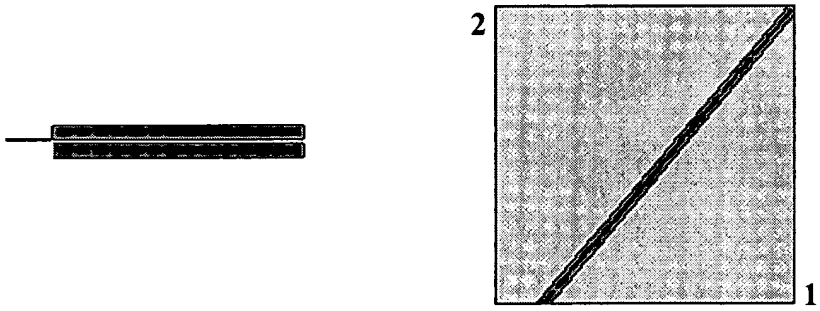
PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ☑ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)

Sequence 2: lcl|seq_2
Length = 639 (1 .. 639)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

```
 Score = 1281 bits (3314),  Expect = 0.0
Identities = 636/639 (99%), Positives = 637/639 (99%), Gaps = 0/639 (0%)

Query  122  LYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSKV  181
            LYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVEN+FREFKLSKV
Sbjct  1    LYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENEFREFKLSKV  60

Query  182  WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK  241
            WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK
Sbjct  61   WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK  120

Query  242  DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA  301
            DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA
Sbjct  121  DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA  180

Query  302  HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS  361
            HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS
Sbjct  181  HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS  240
```

SEQIDNO 1 20

```
Query  362  TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV  421
            TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
Sbjct  241  TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV  300

Query  422  GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY  481
            GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
Sbjct  301  GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY  360

Query  482  INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA  541
            INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA
Sbjct  361  INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA  420

Query  542  FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL  601
            FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
Sbjct  421  FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL  480

Query  602  THDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG  661
            THDVELNLDYE YNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
Sbjct  481  THDVELNLDYEEYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG  540

Query  662  NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ  721
            NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ
Sbjct  541  NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ  600

Query  722  NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  760
            NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct  601  NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  639


CPU time:     0.03 user secs.       0.00 sys. secs          0.03 total secs.

Lambda     K      H
   0.318    0.135    0.399

Gapped
Lambda     K      H
   0.267   0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 3738
Number of extensions: 2121
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 ( 7.3 bits)
X2: 38 (14.6 bits)
```

```
X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)
```

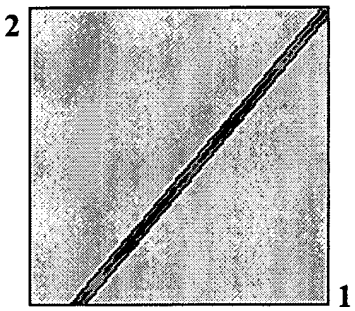
Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ☑ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)

Sequence 2: lcl|seq_2
Length = 639 (1 .. 639)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

```
 Score = 1281 bits (3314),  Expect = 0.0
 Identities = 636/639 (99%), Positives = 637/639 (99%), Gaps = 0/639 (0%)
```

SEQIDNO
1
2

```
Query  122  LYWDDLKRKLSEKLDSTDFTGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSKV  181
            LYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVEN+FREFKLSKV
Sbjct  1    LYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENEFREFKLSKV  60

Query  182  WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK  241
            WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK
Sbjct  61   WRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK  120

Query  242  DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA  301
            DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA
Sbjct  121  DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA  180

Query  302  HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS  361
            HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS
Sbjct  181  HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS  240
```

```
Query  362  TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV  421
            TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV
Sbjct  241  TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGV  300

Query  422  GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY  481
            GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
Sbjct  301  GTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY  360

Query  482  INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA  541
            INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA
Sbjct  361  INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA  420

Query  542  FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL  601
            FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
Sbjct  421  FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL  480

Query  602  THDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG  661
            THDVELNLDYE YNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
Sbjct  481  THDVELNLDYEEYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG  540

Query  662  NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ  721
            NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ
Sbjct  541  NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQ  600

Query  722  NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  760
            NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct  601  NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF  639


CPU time:     0.03 user secs.       0.01 sys. secs          0.04 total secs.

Lambda     K      H
   0.318    0.135    0.399

Gapped
Lambda     K      H
   0.267   0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 3738
Number of extensions: 2121
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 ( 7.3 bits)
X2: 38 (14.6 bits)
```

```
X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)
```

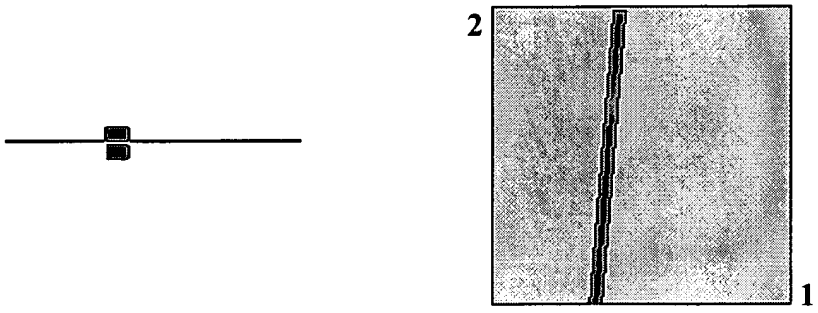
NCBI Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ☑ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)

Sequence 2: gi|2144140|pir||S68317transferrin receptor - guinea pig (fragment)
>gi|1336700|gb|AAB35972.1| transferrin receptor; TfR [Cavia]
Length = 63 (1 .. 63)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

```
 Score =  118 bits (295),  Expect = 2e-24
 Identities = 54/63 (85%), Positives = 57/63 (90%), Gaps = 0/63 (0%)

Query  261  KITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHAHLGTGDPYTPGFPSFNHTQ  320
            KITFAEKVANAESLNA+GVLIY+D TKFPI  A+L  FGH HLGTGDPYTPGFPSFNHTQ
Sbjct  1    KITFAEKVANAESLNALGVLIYLDWTKFPIPKADLPVFGHVHLGTGDPYTPGFPSFNHTQ  60

Query  321  FPP  323
            FPP
Sbjct  61   FPP  63


CPU time:      0.03 user secs.       0.01 sys. secs          0.04 total secs.

Lambda     K      H
```

SEQIDNO 1 22

```
   0.318    0.135    0.399

Gapped
Lambda      K       H
   0.267   0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 413
Number of extensions: 242
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 ( 7.3 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)
```

Blast 2 Sequences results

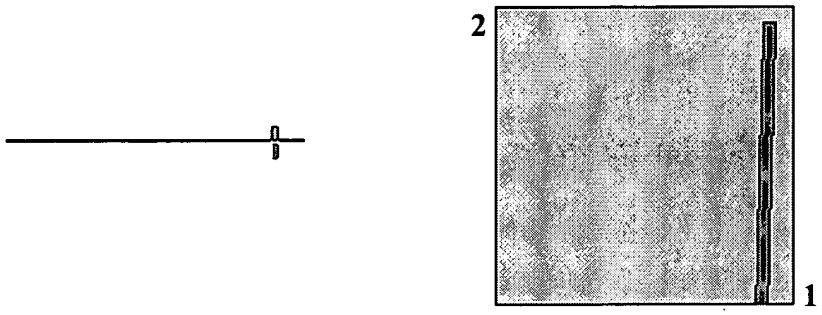
PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☑ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)

Sequence 2: gi|254113|gb|AAB22984.1|transferrin receptor [human, Peptide Partial, 17 aa]
Length = 17 (1 .. 17)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

Score = 40.4 bits (93), Expect = 0.60
SEQIDNO Identities = 17/17 (100%), Positives = 17/17 (100%), Gaps = 0/17 (0%)
1

```
Query  680  RVEYHFLSPYVSPKESP  696
            RVEYHFLSPYVSPKESP
Sbjct  1    RVEYHFLSPYVSPKESP  17
```

23

```
CPU time:     0.03 user secs.       0.01 sys. secs          0.04 total secs.

Lambda      K       H
   0.318    0.135    0.399

Gapped
Lambda      K       H
   0.267   0.0410    0.140
```

```
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 79
Number of extensions: 46
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 ( 7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)
```

Blast 2 Sequences results

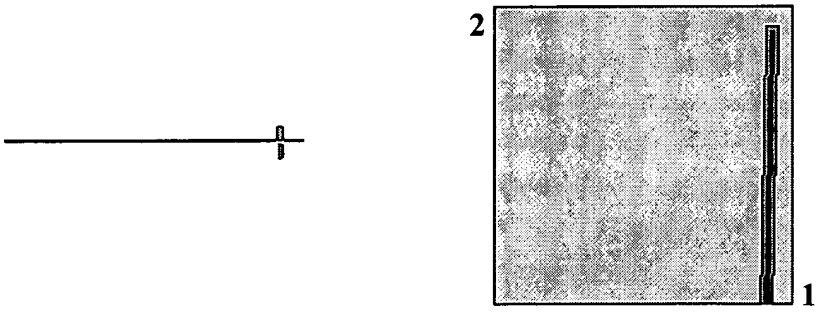
PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☑ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)

Sequence 2: gi|957304|gb|AAB34741.1|transferrin receptor p95, TfR p95 {internal fragment} [human, prostatic-carcinoma cell line DU 145, Peptide Partial, 15 aa, segment 2 of 2]
Length = 15 (1 .. 15)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

```
 Score = 38.9 bits (89),  Expect = 1.7
 Identities = 15/15 (100%), Positives = 15/15 (100%), Gaps = 0/15 (0%)

Query  694  ESPFRHVFWGSGSHT  708
            ESPFRHVFWGSGSHT
Sbjct  1    ESPFRHVFWGSGSHT  15


CPU time:     0.04 user secs.       0.01 sys. secs          0.05 total secs.

Lambda      K       H
   0.318    0.135    0.399

Gapped
Lambda      K       H
```

SEQ ID NO 1 24

```
   0.267    0.0410     0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 74
Number of extensions: 45
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 ( 7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)
```

Blast 2 Sequences results

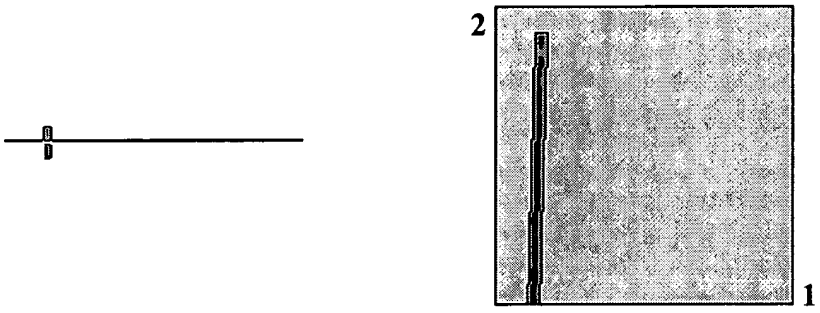
PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 100 expect: 10.000 wordsize: 3 Filter ☑ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)

Sequence 2: gi|233761|gb|AAB19499.1|transferrin receptor [human, K562 erythroleukemia cells, Peptide Partial, 23 aa]
Length = 23 (1 .. 23)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

```
 Score = 37.7 bits (86),  Expect = 3.9
 Identities = 18/22 (81%), Positives = 18/22 (81%), Gaps = 0/22 (0%)
SEQ ID NO
1   Query  101  LAGTESPVREEPGEDFPAARRL  122
               LAG ESPV EEP EDFPAA RL
25  Sbjct  1    LAGKESPVVEEPXEDFPAAXRL  22


CPU time:      0.03 user secs.       0.00 sys. secs          0.03 total secs.

Lambda      K       H
   0.318    0.135    0.399

Gapped
Lambda      K       H
```

```
    0.267    0.0410     0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 108
Number of extensions: 69
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 ( 7.3 bits)
X2: 259 (99.8 bits)
X3: 259 (99.8 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)
```

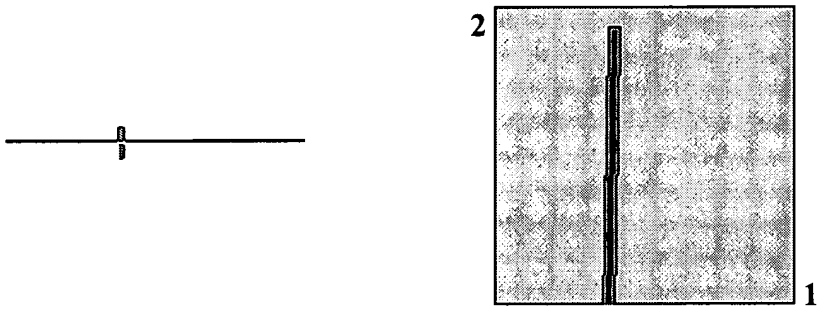
Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 10 gap extension: 2
x_dropoff: 200 expect: 10.000 wordsize: 3 Filter ☑ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)

Sequence 2: gi|957302|gb|AAB34739.1|transferrin receptor p95, TfR p95 {internal fragment} [human, prostatic-carcinoma cell line DU 145, Peptide Partial, 15 aa, segment 1 of 2]
Length = 15 (1 .. 15)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

```
 Score = 38.2 bits (82),  Expect = 3.1
 Identities = 15/15 (100%), Positives = 15/15 (100%), Gaps = 0/15 (0%)

Query  288  FPIVNAELSFFGHAH  302
            FPIVNAELSFFGHAH
Sbjct  1    FPIVNAELSFFGHAH  15


CPU time:      0.04 user secs.       0.01 sys. secs          0.05 total secs.

Lambda      K       H
   0.318    0.135    0.399

Gapped
Lambda      K       H
```

SEQIDNO 1 26

0.291 0.0750 0.230

Matrix: BLOSUM62
Gap Penalties: Existence: 10, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 77
Number of extensions: 50
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 96
Effective length of query: 664
Effective length of database: 1,433,654,294
Effective search space: 951946451216
Effective search space used: 951946451216
Neighboring words threshold: 9
X1: 16 (7.3 bits)
X2: 476 (199.8 bits)
X3: 476 (199.8 bits)
S1: 41 (21.7 bits)
S2: 78 (36.5 bits)